



028723-385.ST25

SEQUENCE LISTING

<110> Tobin, Allan J.
Erlander, Mark G.
Kaufman, Daniel L.

<120> Cloned Glumatic Acid Decarboxylase

<130> 028723-385

<140> US 10/641,149

<141> 2003-08-15

<150> US 07/586,536

<151> 1990-09-12

<160> 8

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<212> PRT

<213> Felis

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<212> PRT

<213> Mus musculus

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<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(1758)

<400> 4

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35 40 45

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Ser Cys Pro Lys Gly Asp Val Asn Tyr Ala Leu Leu His Ala Thr Asp	
85 90 95	
ctg ctg cca gcc tgt gaa gga gaa agg ccc act ctc gca ttt ctg caa	336
Leu Leu Pro Ala Cys Glu Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln	
100 105 110	
gat gta atg aac att ttg ctt cag tac gtg gtg aaa agt ttt gat aga	384
Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg	
115 120 125	
tca act aaa gtg att gat ttc cat tac ccc aat gag ctt ctt caa gag	432
Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu	
130 135 140	
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Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu	
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180 185 190	
gca gat tgg ttg aca tca aca gca aac acg aac atg ttt acc tat gag	624
Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu	
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atc gcc cct gta ttt gta cta ctg gaa tat gtg aca cta aag aaa atg	672
Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met	
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agg gaa atc att ggc tgg cca gga ggc tct ggc gat gga atc ttt tct	720
Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser	
225 230 235 240	
cct ggt ggt gcc atc tcc aac atg tac gcc atg ctc att gcc cgc tat	768
Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Leu Ile Ala Arg Tyr	
245 250 255	
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Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Val Pro Arg	
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275 280 285	
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gga acc act gtg tac ggg gct ttt gat cct ctc ttg gct gta gct gac Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp 340 345 350			1056
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gag agg gcc aac tct gtg aca tgg aat ccc cac aag atg atg ggt gtc Glu Arg Ala Asn Ser Val Thr Trp Asn Pro His Lys Met Met Gly Val 385 390 395 400			1200
ccc ttg caa tgt tct gct ctc ctg gtc aga gag gag gga ctg atg cag Pro Leu Gln Cys Ser Ala Leu Leu Val Arg Glu Glu Gly Leu Met Gln 405 410 415			1248
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cac gtc gat gtc ttt aaa tta tgg ctc atg tgg aga gca aag ggg act His Val Asp Val Phe Lys Leu Trp Leu Met Trp Arg Ala Lys Gly Thr 450 455 460			1392
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ggg aag cct cag cac aca aat gtc tgc ttc tgg ttt gta cct cct agt Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Phe Val Pro Pro Ser 500 505 510			1536
ttg cga gtt ctg gaa gac aat gaa gag aga atg agc cgc ctc tca aag Leu Arg Val Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys 515 520 525			1584
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Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met
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gtc agc tac caa ccc tta gga gat aag gtc aac ttc ttc cgc atg gtc 1680
Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn Phe Phe Arg Met Val
545                               550                               555                               560

atc tca aac cct gca gca act cac caa gac att gac ttc ctc att gaa 1728
Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu
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gaa atc gaa cgc ctg gga caa gat ttg taa 1758
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<210> 5
<211> 585
<212> PRT
<213> Mus musculus

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35      40      45
Tyr Gly Asp Ser Glu Lys Pro Ala Glu Ser Gly Gly Ser Val Thr Ser
50      55      60
Arg Ala Ala Thr Arg Lys Val Ala Cys Thr Cys Asp Gln Lys Pro Cys
65      70      75      80
Ser Cys Pro Lys Gly Asp Val Asn Tyr Ala Leu Leu His Ala Thr Asp
85      90      95
Leu Leu Pro Ala Cys Glu Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln
100      105      110
Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg
115      120      125
Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu
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Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu
145      150      155      160
Thr His Cys Gln Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro
165      170      175
Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala
180      185      190
Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu
195      200      205
Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met
210      215      220
Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser
225      230      235      240
Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Leu Ile Ala Arg Tyr
245      250      255
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Val Pro Arg
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Gly Thr Thr Val Tyr Gly	Ala Phe Asp Pro Leu	Leu Ala Val Ala Asp
340	345	350
Ile Cys Lys Lys Tyr Lys	Ile Trp Met His Val	Asp Ala Ala Trp Gly
355	360	365
Gly Gly Leu Leu Met Ser	Arg Lys His Lys Trp	Lys Leu Asn Gly Val
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Glu Arg Ala Asn Ser Val	Thr Trp Asn Pro His	Lys Met Met Gly Val
385	390	395
Pro Leu Gln Cys Ser Ala	Leu Leu Val Arg Glu	Glu Gly Leu Met Gln
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Ser Cys Asn Gln Met His	Ala Ser Tyr Leu Phe	Gln Gln Asp Lys His
420	425	430
Tyr Asp Leu Ser Tyr Asp	Thr Gly Asp Lys Ala	Leu Gln Cys Gly Arg
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His Val Asp Val Phe Lys	Leu Trp Leu Met Trp	Arg Ala Lys Gly Thr
450	455	460
Thr Gly Phe Glu Ala His	Ile Asp Lys Cys Leu	Glu Leu Ala Glu Tyr
465	470	475
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Gly Lys Pro Gln His Thr	Asn Val Cys Phe Trp	Phe Val Pro Pro Ser
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Leu Arg Val Leu Glu Asp	Asn Glu Arg Met Ser	Arg Leu Ser Lys
515	520	525
Val Ala Pro Val Ile Lys	Ala Arg Met Met Glu	Tyr Gly Thr Thr Met
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 <212> DNA
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<220>
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 <222> (1)...(1758)

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tct ggg gat tcc gag aat ccc ggc aca gcg cga gcc tgg tgc caa gtg 96
Ser Gly Asp Ser Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val
          20             25            30

gct cag aag ttc acg ggc ggc atc gga aac aaa ctg tgc gcc ctg ctc 144
Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu
          35             40            45

tac gga gac gcc gag aag ccg gcg gag agc ggc ggg agc caa ccc ccg 192
Tyr Gly Asp Ala Glu Lys Pro Ala Glu Ser Gly Gly Ser Gln Pro Pro
          50             55            60

cgg gcc gcc gcc ccg aag gcc gcc tgc gcc tgc gac cag aag ccc tgc 240
Arg Ala Ala Ala Arg Lys Ala Ala Cys Ala Cys Asp Gln Lys Pro Cys
          65             70            75            80

agc tgc tcc aaa gtg gat gtc aac tac gcg ttt ctc cat gca aca gac 288
Ser Cys Ser Lys Val Asp Val Asn Tyr Ala Phe Leu His Ala Thr Asp
          85             90            95

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Leu Leu Pro Ala Cys Asp Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln

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115	120 125														
tca acc aaa gtg att gat ttc cat tat cct aat gag ctt ctc caa gaa	432														
Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu															
130	135 140														
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Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu															
145	150 155 160														
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Met His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro															
165	170 175														
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Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu															
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Ile Ala Pro Val Phe Val Leu Leu Glu Tyr Val Thr Leu Lys Lys Met															
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Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser															
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245	250 255														
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Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg															
260	265 270														
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Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly															
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Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys															
290	295 300														
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305	310 315 320														
gaa gcc aaa cag aaa ggg ttt gtt cct ttc ctc gtg agt gcc aca gct	1008														
Glu Ala Lys Gln Lys Gly Phe Val Pro Phe Leu Val Ser Ala Thr Ala															
325	330 335														
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Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp	
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Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly	
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ggg gga tta ctg atg tcc cga aaa cac aag tgg aaa ctg agt ggc gtg	1152
Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Ser Gly Val	
370 375 380	
gag agg gcc aac tct gtg acg tgg aat cca cac aag atg atg gga gtc	1200
Glu Arg Ala Asn Ser Val Thr Trp Asn Pro His Lys Met Met Gly Val	
385 390 395 400	
cct ttg cag tgc tct gct ctc ctg gtt aga gaa gag gga ttg atg cag	1248
Pro Leu Gln Cys Ser Ala Leu Leu Val Arg Glu Glu Gly Leu Met Gln	
405 410 415	
aat tgc aac caa atg cat gcc tcc tac ctc ttt cag caa gat aaa cat	1296
Asn Cys Asn Gln Met His Ala Ser Tyr Leu Phe Gln Gln Asp Lys His	
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tat gac ctg tcc tat gac act gga gac aag gcc tta cag tgc gga cgc	1344
Tyr Asp Leu Ser Tyr Asp Thr Gly Asp Lys Ala Leu Gln Cys Gly Arg	
435 440 445	
cac gtt gat gtt ttt aaa cta tgg ctg atg tgg agg gca aag ggg act	1392
His Val Asp Val Phe Lys Leu Trp Leu Met Trp Arg Ala Lys Gly Thr	
450 455 460	
acc ggg ttt gaa gcg cat gtt gat aaa tgt ttg gag ttg gca gag tat	1440
Thr Gly Phe Glu Ala His Val Asp Lys Cys Leu Glu Leu Ala Glu Tyr	
465 470 475 480	
tta tac aac atc ata aaa aac cga gaa gga tat gag atg gtg ttt gat	1488
Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp	
485 490 495	
ggg aag cct cag cac aca aat gtc tgc ttc tgg tac att cct cca agc	1536
Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser	
500 505 510	
ttg cgt act ctg gaa gac aat gaa gag aga atg agt cgc ctc tcg aag	1584
Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys	
515 520 525	
gtg gct cca gtg att aaa gcc aga atg atg gag tat gga acc aca atg	1632
Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met	
530 535 540	
gtc agc tac caa ccc ttg gga gac aag gtc aat ttc ttc cgc atg gtc	1680
Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn Phe Phe Arg Met Val	
545 550 555 560	
atc tca aac cca gcg gca act cac caa gac att gac ttc ctg att gaa	1728
Ile Ser Asn Pro Ala Ala Thr His Gln Asp Ile Asp Phe Leu Ile Glu	
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gaa ata gaa cgc ctt gga caa gat tta taa
 Glu Ile Glu Arg Leu Gly Gln Asp Leu *
 580 585

1758

<210> 8
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 <212> PRT
 <213> Homo sapiens

<400> 8
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 1 5 10 15
 Ser Gly Asp Ser Glu Asn Pro Gly Thr Ala Arg Ala Trp Cys Gln Val
 20 25 30
 Ala Gln Lys Phe Thr Gly Gly Ile Gly Asn Lys Leu Cys Ala Leu Leu
 35 40 45
 Tyr Gly Asp Ala Glu Lys Pro Ala Glu Ser Gly Gly Ser Gln Pro Pro
 50 55 60
 Arg Ala Ala Ala Arg Lys Ala Ala Cys Ala Cys Asp Gln Lys Pro Cys
 65 70 75 80
 Ser Cys Ser Lys Val Asp Val Asn Tyr Ala Phe Leu His Ala Thr Asp
 85 90 95
 Leu Leu Pro Ala Cys Asp Gly Glu Arg Pro Thr Leu Ala Phe Leu Gln
 100 105 110
 Asp Val Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp Arg
 115 120 125
 Ser Thr Lys Val Ile Asp Phe His Tyr Pro Asn Glu Leu Leu Gln Glu
 130 135 140
 Tyr Asn Trp Glu Leu Ala Asp Gln Pro Gln Asn Leu Glu Glu Ile Leu
 145 150 155 160
 Met His Cys Gln Thr Thr Leu Lys Tyr Ala Ile Lys Thr Gly His Pro
 165 170 175
 Arg Tyr Phe Asn Gln Leu Ser Thr Gly Leu Asp Met Val Gly Leu Ala
 180 185 190
 Ala Asp Trp Leu Thr Ser Thr Ala Asn Thr Asn Met Phe Thr Tyr Glu
 195 200 205
 Ile Ala Pro Val Phe Val Leu Glu Tyr Val Thr Leu Lys Lys Met
 210 215 220
 Arg Glu Ile Ile Gly Trp Pro Gly Gly Ser Gly Asp Gly Ile Phe Ser
 225 230 235 240
 Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe
 245 250 255
 Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
 260 265 270
 Leu Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Gly
 275 280 285
 Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Leu Ile Lys Cys
 290 295 300
 Asp Glu Arg Gly Lys Met Ile Pro Ser Asp Pro Glu Arg Arg Ile Leu
 305 310 315 320
 Glu Ala Lys Gln Lys Gly Phe Val Pro Phe Leu Val Ser Ala Thr Ala
 325 330 335
 Gly Thr Thr Val Tyr Gly Ala Phe Asp Pro Leu Leu Ala Val Ala Asp
 340 345 350
 Ile Cys Lys Lys Tyr Lys Ile Trp Met His Val Asp Ala Ala Trp Gly
 355 360 365
 Gly Gly Leu Leu Met Ser Arg Lys His Lys Trp Lys Leu Ser Gly Val
 370 375 380

Glu	Arg	Ala	Asn	Ser	Val	Thr	Trp	Asn	Pro	His	Lys	Met	Met	Gly	Val	385	390	395	400
Pro	Leu	Gln	Cys	Ser	Ala	Leu	Leu	Val	Arg	Glu	Glu	Gly	Leu	Met	Gln	405	410	415	
Asn	Cys	Asn	Gln	Met	His	Ala	Ser	Tyr	Leu	Phe	Gln	Gln	Asp	Lys	His	420	425	430	
Tyr	Asp	Leu	Ser	Tyr	Asp	Thr	Gly	Asp	Lys	Ala	Leu	Gln	Cys	Gly	Arg	435	440	445	
His	Val	Asp	Val	Phe	Lys	Leu	Trp	Leu	Met	Trp	Arg	Ala	Lys	Gly	Thr	450	455	460	
Thr	Gly	Phe	Glu	Ala	His	Val	Asp	Lys	Cys	Leu	Glu	Leu	Ala	Glu	Tyr	465	470	475	480
Leu	Tyr	Asn	Ile	Ile	Lys	Asn	Arg	Glu	Gly	Tyr	Glu	Met	Val	Phe	Asp	485	490	495	
Gly	Lys	Pro	Gln	His	Thr	Asn	Val	Cys	Phe	Trp	Tyr	Ile	Pro	Pro	Ser	500	505	510	
Leu	Arg	Thr	Leu	Glu	Asp	Asn	Glu	Glu	Arg	Met	Ser	Arg	Leu	Ser	Lys	515	520	525	
Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Thr	Met	530	535	540	
Val	Ser	Tyr	Gln	Pro	Leu	Gly	Asp	Lys	Val	Asn	Phe	Phe	Arg	Met	Val	545	550	555	560
Ile	Ser	Asn	Pro	Ala	Ala	Thr	His	Gln	Asp	Ile	Asp	Phe	Leu	Ile	Glu	565	570	575	
Glu	Ile	Glu	Arg	Leu	Gly	Gln	Asp	Leu								580	585		